

Art Unit: 1631

p. 26 line 4 - pg. 26. line 12

--Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(on the world wide web at ddbj.nig.ac.jp/); Genebank (on the world wide web at ncbi.nlm.nih.gov/Web/Search/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (on the world wide web at ebi.ac.uk/ebi_docs/embl_db/embl-db.html). Other appropriate databases include dbEST (on the world wide web at ncbi.nlm.nih.gov/dbEST/index.html), SwissProt (on the world wide web at ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html), PIR (on the world wide web at nbri.georgetown.edu/pir/) and The Institute for Genome Research (on the world wide web at tigr.org/tdb/tdb.html).--

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10/13/08

(C) In the Claims, please replace the following:

“Claim 24. A plant genome comprising the recombinant nucleic acid construct of claim 23.”

with

--Claim 24. (Currently Amended) A transformed plant comprising a nucleic acid molecule which comprises:

(a) an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule; which is linked to;

(b) a nucleic acid molecule, wherein said nucleic acid molecule comprises a nucleic acid sequence that shares between 100% and 90% sequence identity with SEQ ID NO: 1 or the complete complement thereof, which is linked to

(c) a 3' non-translated sequence that functions in said plant cell to cause the termination of transcription and the addition of polyadenylated ribonucleotides to said 3' end of said mRNA molecule.--